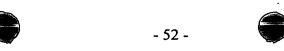
20

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(1) GENERAL INFORMATION:

(i) APPLICANT: Bujard, Hermann
 Gossen, Manfred
 Salfeld, Jochen G.
 Voss, Jeffrey W.

(ii) TITLE OF INVENTION: Methods for Regulating Gene Expression

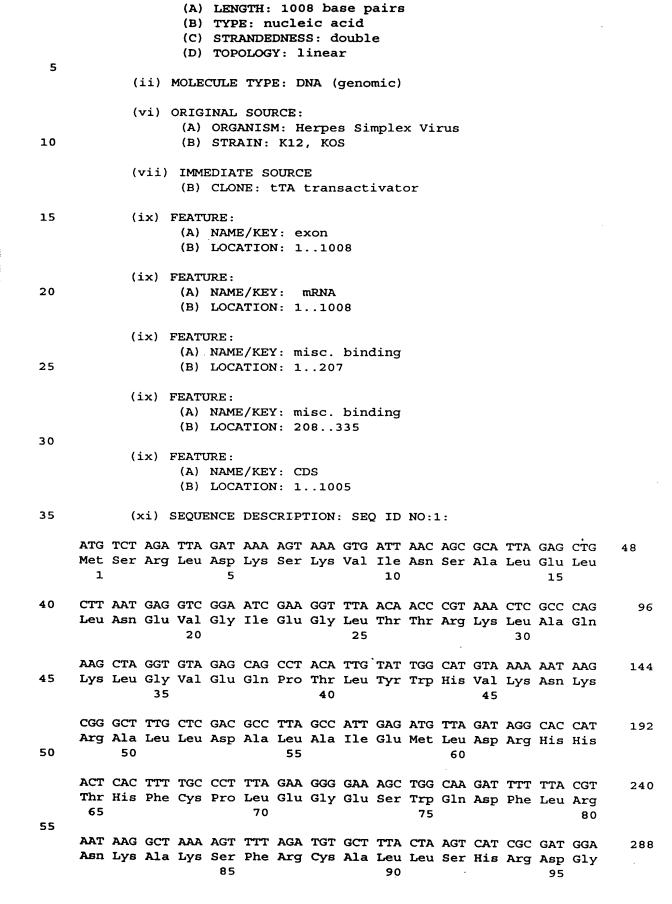
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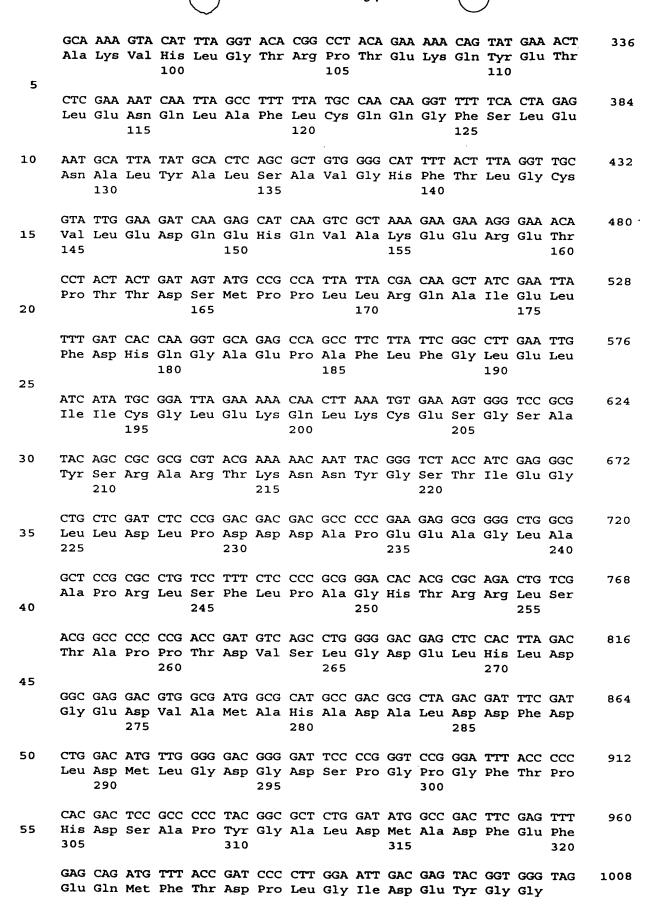
- 10 (iii) NUMBER OF SEQUENCES: 10
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Lahive & Cockfield
 - (B) STREET: 60 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: ASCII text
- 25 (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/383,754
 - (B) FILING DAE: 14-JUN-1994
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/076,327
 - (B) FILING DAE: 14-JUN-1993
- 35 (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: DeConti, Giulio A., Jr.
 - (B) REGISTRATION NUMBER: 31,503
 - (C) REFERENCE/DOCKET NUMBER: BBI-013CP3
- 40 (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 227-7400
 - (B) TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:





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The first three that the first two the first first

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(2) INFORMATION FOR SEQ ID NO:2:

(i	.)	SEQUENCE	CHARACTERISTICS:
	.,		CIMUCI DRIBLICS.

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10	Met	Ser	Arg	Leu	Asp	Lys	Ser	Lys	Val	Ile	Asn	Ser	Ala	Leu	Glu	Leu
	1				5					10					15	

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys 35 40 45

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His 20 50 55 60

Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 65 70 75 80

25 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 35 130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 145 150 155 160

40 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu 165 170 175

Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu 180 185 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala 195 200 205

Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly 210 215 220

Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala 225 230 235 240

55 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser

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245 250 255 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp 265 5 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp 280 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro 10 295 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe 310 315 15 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly (2) INFORMATION FOR SEQ ID NO:3: 20 (i) SEQUENCE CHARACTERISTICS:

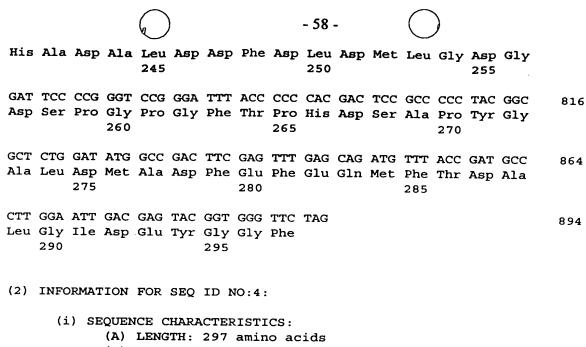
- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Herpes Simplex Virus
- (B) STRAIN: K12, KOS
 - (C) INDIVIDUAL ISOLATE: tTAS transactivator
 - (ix) FEATURE:
 - (A) NAME/KEY: exon
- 35 (B) LOCATION: 1..894
 - (ix) FEATURE:
 - (A) NAME/KEY: mRNA
 - (B) LOCATION: 1..894
 - (ix) FEATURE:
 - (A) NAME/KEY: misc. binding
 - (B) LOCATION: 1..207
- 45 (ix) FEATURE:
 - (A) NAME/KEY: misc. binding
 - (B) LOCATION: 208..297
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..891
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
- ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG 55 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu

1 10 15 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 96 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln AAG CTA GGT GTA GAG CAG CCT ACA TTG TAT TGG CAT GTA AAA AAT AAG 144 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT 192 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His 10 55 ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT 240 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg AAT AAC GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA 288 Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 90 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 100 20 CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG 384 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 115 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC 432 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 25 130 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA 480 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 145 150 CCT ACT ACT GAT AGT CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA 528 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu 3.0 165 TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG 576 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu 185 ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCT GAT 35 624 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Asp 195 CCA TCG ATA CAC ACG CGC AGA CTG TCG ACG GCC CCC CCG ACC GAT GTC 672 Pro Ser Ile His Thr Arg Arg Leu Ser Thr Ala Pro Pro Thr Asp Val 40 210 215 AGC CTG GGG GAC GAG CTC CAC TTA GAC GGC GAG GAC GTG GCG ATG GCG 720 Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp Val Ala Met Ala 225 230 235 CAT GCC GAC GCG CTA GAC GAT TTC GAT CTG GAC ATG TTG GGG GAC GGG 768

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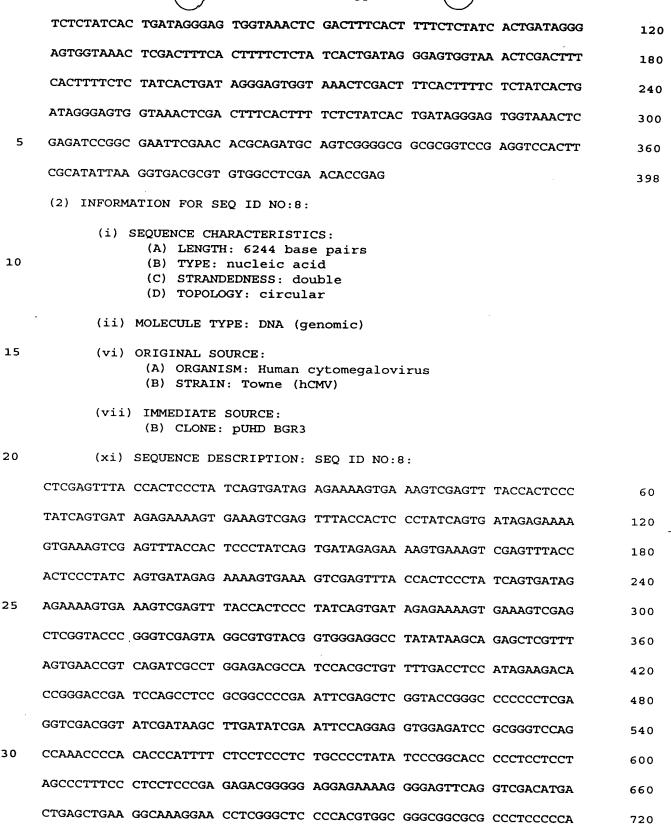


- (B) TYPE: amino acid.
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
- Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu 20 1 5 10 15
 - Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
 20 25 30
- 25 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys 35 40 45
 - Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His 50 55 60
 - Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
 65 70 75 80
- Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
 85 90 95
 - Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
- 40 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 115 120 125
 - Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 130 135 140
 - Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 145 150 155 160
- Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu 50 165 170 175

	Phe	Asp	His	Gln 180	Gly	Ala	Glu	Pro	Ala 185		Leu	Phe	Gly	Leu 190	Glu	Leu		
5	Ile	Ile	Сув 195	Gly	Leu	Glu	Lys	Gln 200	Leu	Lys	Cys	Glu	Ser 205	Gly	Ser	Asp		
10	Pro	Ser 210	Ile	His	Thr	Arg 215	Arg	Leu	Ser	Thr	Ala	Pro 220	Pro	Thr	Asp	Val		
	Ser 225	Leu	Gly	Asp	Glu	Leu 230	His	Leu	Asp	Gly	Glu 235	Asp	Val	Ala	Met	Ala 240		
15	His	Ala	Asp	Ala	Leu 245	Asp	Asp	Phe	Asp	Leu 250	Asp	Met	Leu	Gly	Asp 255	Gly		
	Asp	Ser	Pro	Gly 260	Pro	Gly	Phe	Thr	Pro 265	His	Asp	Ser	Ala	Pro 270	Tyr	Gly		
20	Ala	Leu	Asp 275	Met	Ala	Asp	Phe	Glu 280	Phe	Glu	Gln	Met	Phe 285	Thṛ	Asp	Ala	,	
25	Leu	Gly 290	Ile	Asp	Glu	Tyr	Gly 295	Gly	Phe									
	(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	iO : 5 :										
30		(i	.) SE	(B) (C)	LENG TYPE STRA	TH: : nu NDED	CTER 450 clei NESS	base c ac	e pai id ouble									
35		(i	i) M	OLEC						nic)								
		(√	ri) C		ORGA	NISM				mega	lovi	rus						
40		(i	•	EATU	RE:	/KEY		AM										
		(x	i) S	EQUE	NCE	DESC	RIPT	'ION :	SEÇ	D	NO:5	i:						
45	GAAT	TCCI	CG A	GTTI	'ACCA	C TC	CCTA	TCAG	TGA	TAGA	GAA	AAGT	GAAA	GT C	GAGT	TTACC		60
	ACTO	CCTA	ATC A	GTGA	TAGA	G AA	AAGT	'GAAA	GTC	GAGT	TTA	CCAC	TCCC	TA T	'CAGT	GATAG		120
	AGAA	LAAGI	GA A	AGTO	GAG1	T TA	CCAC	TCCC	TAT	CAGI	'GAT	AGAG	AAAA	GT G	AAAG	TCGAG		180
	TTTA	CCAC	CTC C	CTAT	CAGI	G AT	'AGAG	AAAA	GTG	AAAG	TCG	AGTT	TACC	AC I	CCCI	TATCAG		240
	TGAT	AGAG	AA A	AGTO	AAAG	T CG	AGTI	TACC	ACI	CCCI	ATC	AGTG	ATAG	AG A	AAAG	TGAAA		300
50	GTCG	AGCI	CG G	TACC	CGGC	T CG	AGTA	GGCG	TGI	'ACGG	TGG	GAGG	CCTA	та т	אמכר'	'AGAGC		360

	TCGTTTAGTG AACCGTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTTG ACCTCCATAG	420
	AAGACACCGG GACCGATCCA GCCTCCGCGG	450
	(2) INFORMATION FOR SEQ ID NO:6:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:(A) ORGANISM: Human cytomegalovirus(B) STRAIN: Towne	
15	(ix) FEATURE: (A) NAME/KEY: mRNA (B) LOCATION: 382450	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	GAATTCCTCG ACCCGGGTAC CGAGCTCGAC TTTCACTTTT CTCTATCACT GATAGGGAGT	60
	GGTAAACTCG ACTTTCACTT TTCTCTATCA CTGATAGGGA GTGGTAAACT CGACTTTCAC	120
	TTTTCTCTAT CACTGATAGG GAGTGGTAAA CTCGACTTTC ACTTTTCTCT ATCACTGATA	180
	GGGAGTGGTA AACTCGACTT TCACTTTTCT CTATCACTGA TAGGGAGTGG TAAACTCGAC	240
25	TTTCACTTTT CTCTATCACT GATAGGGAGT GGTAAACTCG ACTTTCACTT TTCTCTATCA	300
	CTGATAGGGA GTGGTAAACT CGAGTAGGCG TGTACGGTGG GAGGCCTATA TAAGCAGAGC	360
	TCGTTTAGTG AACCGTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTTG ACCTCCATAG	420
	AAGACACCGG GACCGATCCA GCCTCCGCGG	450
	(2) INFORMATION FOR SEQ ID NO:7:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 398 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:(A) ORGANISM: Herpes Simplex Virus(B) STRAIN: KOS	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
	GAGCTCGACT TTCACTTTC TCTATCACTG ATAGGGAGTG GTAAACTCGA CTTTCACTTT	60

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CCGAGGTCGG ATCCCAGCTC CTGGGTCGCC CGGACCCTGG CCCCTTCCAG GGGAGCCAGA

CCTCAGAGGC CTCGTCTGTA GTCTCCGCCA TCCCCATCTC CCTGGACGGG TTGCTCTTCC

780







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CGTC

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4963 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human cytomegalovirus
 - (vii) IMMEDIATE SOURCE:

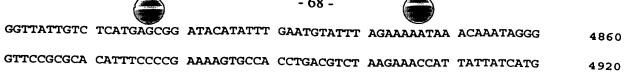
(B) CLONE: pUHD BGR4

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCGAGTTTA CCACTCCCTA TCAGTGATAG AGAAAAGTGA AAGTCGAGTT TACCACTCCC 60 TATCAGTGAT AGAGAAAAGT GAAAGTCGAG TTTACCACTC CCTATCAGTG ATAGAGAAAA 120 GTGAAAGTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC 180 ACTCCCTATC AGTGATAGAG AAAAGTGAAA GTCGAGTTTA CCACTCCCTA TCAGTGATAG 240 AGAAAAGTGA AAGTCGAGTT TACCACTCCC TATCAGTGAT AGAGAAAAGT GAAAGTCGAG 300 CTCGGTACCC GGGTCGAGTA GGCGTGTACG GTGGGAGGCC TATATAAGCA GAGCTCGTTT 360 AGTGAACCGT CAGATCGCCT GGAGACGCCA TCCACGCTGT TTTGACCTCC ATAGAAGACA 420 CCGGGACCGA TCCAGCCTCC GCGGCCCCGA ATTCCGGCCA CGACCATGAC CATGACCCTC 480 CACACCAAAG CATCTGGGAT GGCCCTACTG CATCAGATCC AAGGGAACGA GCTGGAGCCC 540 CTGAACCGTC CGCAGCTCAA GATCCCCCTG GAGCGGCCCC TGGGCGAGGT GTACCTGGAC 600 AGCAGCAAGC CCGCCGTGTA CAACTACCCC GAGGGCGCCG CCTACGAGTT CAACGCCGCG 660 GCCGCCGCCA ACGCGCAGGT CTACGGTCAG ACCGGCCTCC CCTACGGCCC CGGGTCTGAG 720 GCTGCGGCGT TCGGCTCCAA CGGCCTGGGG GGTTTCCCCC CACTCAACAG CGTGTCTCCG 780 AGCCCGCTGA TGCTACTGCA CCCGCCGCCG CAGCTGTCGC CTTTCCTGCA GCCCCACGGC 840 CAGCAGGTGC CCTACTACCT GGAGAACGAG CCCAGCGGCT ACACGGTGCG CGAGGCCGGC 900 CCGCCGGCAT TCTACAGGCC AAATTCAGAT AATCGACGCC AGGGTGGCAG AGAAAGATTG 960 GCCAGTACCA ATGACAAGGG AAGTATGGCT ATGGAATCTG CCAAGGAGAC TCGCTACTGT 1020 GCAGTGTGCA ATGACTATGC TTCAGGCTAC CATTATGGAG TCTGGTCCTG TGAGGGCTGC 1080 AAGGCCTTCT TCAAGAAG TATTCAAGGA CATAACGACT ATATGTGTCC AGCCACCAAC 1140 CAGTGCACCA TTGATAAAAA CAGGAGGAAG AGCTGCCAGG CCTGCCGGCT CCGCAAATGC



CGTTCGGCTG CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA 3060 ATCAGGGGAT AACGCAGGAA AGAACATGTG AGCAAAAGGC CAGCAAAAGG CCAGGAACCG 3120 TAAAAAGGCC GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC CCCCCTGACG AGCATCACAA 3180 AAATCGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT 3240 TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA CCGGATACCT 5 3300 GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAA TGCTCACGCT GTAGGTATCT 3360 CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT GGGCTGTGTG CACGAACCCC CCGTTCAGCC 3420 CGACCGCTGC GCCTTATCCG GTAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT 3480 ATCGCCACTG GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC 3540 TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG TATTTGGTAT 10 3600 CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAGCTCTT GATCCGGCAA 3660 ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTTTGCAAG CAGCAGATTA CGCGCAGAAA 3720 AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA 3780 AAACTCACGT TAAGGGATTI TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT 3840 TTTAAATTAA AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA CTTGGTCTGA 15 3900 CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTCATC 3960 CATAGTTGCC TGATCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC 4020 CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATTT ATCAGCAATA 4080 -AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC CGCCTCCATC 4140 CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGCGC 20 4200 AACGTTGTTG CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTTGG TATGGCTTCA 4260 TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA 4320 GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTTATCA 4380 CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT 4440 25 TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT 4500 TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGCGCCAC ATAGCAGAAC TTTAAAAGTG 4560 CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA GGATCTTACCGCTGTTGAGA 4620 TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTCACC 4680 AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG AATAAGGGCG 4740 ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG 30 4800



5 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE	CHARACTERISTICS
	/ DECORNCE	CHARACIERISIICS

(A) LENGTH: 42 base pairs

ACATTAACCT ATAAAAATAG GCGTATCACG AGGCCCTTTC GTC

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCGAGTTTAC CACTCCCTAT CAGTGATAGA GAAAAGTGAA AG

42